Amendments to the Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims

Claim 1 (Currently amended) An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1~~, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, or SEQ ID NO:23~~, or a full complement thereof.

Claim 2 (canceled)

Claim 3 (canceled)

Claim 4 (Currently amended) An isolated nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2~~, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, or SEQ ID NO:24~~.

Claim 5 (Currently amended) An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a Corynebacterium glutamicum polypeptide comprising the amino acid sequence of SEQ ID NO:2~~, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, or SEQ ID NO:24~~, wherein the nucleic acid molecule hybridizes to ~~the~~ a full complement of a nucleic acid molecule consisting of SEQ ID NO:1~~, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, or SEQ ID NO:23~~ in 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C, and wherein said nucleic acid molecule

encodes a polypeptide which is capable of functioning as a protein translation elongation factor G polypeptide.

Claim 6 (Currently amended) An isolated nucleic acid molecule comprising a nucleotide sequence which has at least ~~50~~90% identity with the nucleotide sequence of SEQ ID NO:1~~, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, or SEQ ID NO:23~~, or ~~the~~ a full complement thereof, and wherein said nucleic acid molecule encodes a polypeptide which is capable of functioning as a protein translation elongation factor G polypeptide.

Claim 7 (Currently amended) An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO:1~~, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, or SEQ ID NO:23~~, or ~~the~~ a full complement thereof.

Claim 8 (canceled)

Claim 9 (canceled)

Claim 10 (Original) A vector comprising the nucleic acid molecule of claim 1.

Claim 11 (Original) The vector of claim 10, which is an expression vector.

Claim 12 (Original) A host cell transfected with the expression vector of claim 11.

Claim 13 (Original) The host cell of claim 12, wherein said cell is a microorganism.

Claim 14 (Original) The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

Claim 15 (Original) The host cell of claim 12 or 43, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

Claim 16 (Original) The host cell of claim 15 or 43, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

Claims 17-35 (Canceled)

Claim 36 (Currently amended) A host cell comprising ~~the~~ a nucleic acid molecule comprising a nucleotide sequence derived from ~~of~~ SEQ ID NO:1~~, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, or SEQ ID NO:23~~, or ~~the~~ a full complement thereof, wherein the nucleic acid molecule is disrupted, and wherein the disrupted nucleic acid molecule encodes a polypeptide which is capable of functioning as a protein translation elongation factor G polypeptide.

Claim 37 (Currently amended) A host cell comprising ~~the~~ a nucleic acid molecule comprising a nucleotide sequence derived from ~~of, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, or SEQ ID NO:23~~, or ~~the~~ a full complement thereof, wherein the nucleic acid molecule comprises one or more nucleic acid modifications, and wherein the modified nucleic acid molecule encodes a polypeptide which is capable of functioning as a protein translation elongation factor G polypeptide.

Claim 38 (Currently amended) A host cell comprising ~~the~~ a nucleic acid molecule comprising a nucleotide sequence derived from ~~of, SEQ ID NO:3, SEQ ID NO:5, SEQ~~

~~ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, or SEQ ID NO:23~~, or ~~the~~ a full complement thereof, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule, and wherein the nucleic acid molecule encodes a polypeptide which is capable of functioning as a protein translation elongation factor G polypeptide.

Claim 39 (canceled)

Claim 40 (New) An isolated nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO:1, or a full complement thereof.

Claim 41 (New) An isolated nucleic acid molecule which encodes a polypeptide consisting of the amino acid sequence set forth in SEQ ID NO:2, or a full complement thereof.

Claim 42 (New) An isolated nucleic acid molecule consisting of a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO:1, or a full complement thereof, wherein said nucleotide sequence encodes a polypeptide which is capable of functioning as a protein translation elongation factor G polypeptide.

Claim 43 (New) The host cell of claim 13, wherein said cell is a bacterial cell.

REMARKS

Claims 1-17 and 36-39 were pending the application. Claims 2, 3, 8, 9, 17, and 39 have been canceled, without prejudice, and claims 40, 41, 42, and 43 have been added. Claims 1, 4, 5, 6, 7, 36, 37, and 38 have been amended. Accordingly, upon entry of this amendment, claims 1, 4-7, 10-16, 36-38, and 40-43 will be pending.

Support for the amendments to the claims and the new claims may be found, at least, in the specification and claims as originally filed.

No new matter has been added. Any amendments to and/or cancellation of the claims should in no way be construed as an acquiescence to any of the Examiner's rejections and was done solely to more particularly point out and distinctly claim the subject matter of Applicants' invention in order to expedite the prosecution of the application. Applicants reserve the right to pursue the claims as originally filed in this or a separate application(s).

Information Disclosure Statement

With respect to the Information Disclosure Statement for the instant application, the Examiner has indicated that "[t]he listing of references in the specification is not a proper information disclosure statement. 37 CFR 1.98(b) requires a list of all patents, publications, or other information submitted for consideration by the Office, and MPEP § 609 A(l) states, "the list may not be incorporated into the specification but must be submitted in a separate paper."

Applicants respectfully submit that they intend to file an Information Disclosure Statement for the instant application in due course.

Claim Objections

The Examiner has objected to claims 1, 3, 5-7, and 36-39 because, according to the Examiner, "the phrase "SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, or SEQ ID NO: 23 "

should be deleted and replace with "SEQ ID NO:1" since applicant has selected SEQ ID NO: 1 as the result of the restriction requirement."

Applicants respectfully traverse the foregoing objection to the claims. However, in the interest of expediting prosecution, claim 39 has been canceled and claims 1, 3, 5-7, and 36-38 have been amended as suggested by the Examiner. Accordingly, Applicants respectfully request withdrawal of the foregoing objection to the claims.

The Examiner has also objected to claim 2 because "'SES' is an abbreviation. This phrase can only be used after it appears once."

Applicants respectfully traverse the foregoing objection to claim 2. However, in the interest of expediting prosecution, claim 2 has been cancelled thereby rendering the foregoing objection moot.

The Examiner has also objected to claims 4, 5, and 39 because, according to the Examiner, "the phrase " SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24" should be deleted and replace with "SEQ ID NO:2" since applicant has selected SEQ ID NO: 1 as the result of the restriction requirement and the examiner only agrees to examine SEQ ID NO: 2."

Applicants respectfully traverse the foregoing objection to the claims. However, in the interest of expediting prosecution, claim 39 has been canceled and claims 4 and 5 have been amended as suggested by the Examiner. Accordingly, Applicants respectfully request withdrawal of the foregoing objection to the claims.

Rejection of Claims 1-6, 9-16, and 36-39 Under 35 U.S.C. §112, First Paragraph

The Examiner has rejected claims 1-6, 9-16, and 36-39 under 35 U.S.C. §112, first paragraph, "as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." In particular, the Examiner is of the opinion that

an isolated nucleic acid molecule recited in claims 1-3 and 9-16, and (a) of claim 39 was read as any kind of isolated nucleic acid molecule which had SEQ ID NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1, and could be read as a chromosome having SEQ ID NO: 1. An isolated nucleic acid molecule recited in claim 4 and (c) of claim 39 was read as any kind of isolated nucleic acid molecule which had SEQ ID NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1 and could be read as a chromosome having SEQ ID NO: 1 since this nucleic acid molecule could encode a polypeptide comprising the amino acid sequence of or set forth in SEQ ID NO: 2. An isolated nucleic acid molecule recited in claim 5 and (d) of claim 39 was read as any kind of naturally occurring allelic variant of a nucleic acid molecule which had SEQ ID NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1 wherein the isolated nucleic acid molecule could hybridize to the complement of a nucleic acid molecule consisting of SEQ ID NO: 1 in 6X SSC at 45 °C. An isolated nucleic acid molecule recited in claim 6 and (e) of claim 39 was read as any kind of nucleic acid which has at least 50% identity with the nucleotide sequence comprising SEQ ID No: 1 that had SEQ ID NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1. An isolated nucleic acid molecule recited in kind of isolated nucleic acid comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO: 1 and could be read as a chromosome having at least 15 nucleotides of SEQ ID NO: 1. A host cell recited in claim 36 was read as a host cell comprising any kind of nucleic acid molecule because claim 36 did not limit the extent, percentage, and location of the disruption and the nucleic acid molecule with the disruption was not considered as the same nucleic acid molecule which had SEQ ID NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1. A host cell recited in claim 37 was read as a host cell comprising any kind of nucleic acid molecule because claim 37 did not limit the extent, percentage, and location of the modification and the nucleic acid molecule comprising more nucleic acid modifications as recited in claim 37 was not considered to be the same nucleic acid molecule which had SEQ ID NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1. A host cell recited in claim 38 was read as a host cell comprising any kind of nucleic acid molecule because claim 38 did not limit the extent, percentage and location of the modification and the nucleic acid molecule comprising the modifications on the regulatory region as recited in claim 38 was not considered to be the same nucleic acid molecule which had SEQ ID

> NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1. Although the specification adequately describes an isolated nucleic acid consisting of the nucleotide sequence of SEQ ID No: 1 and its corresponding protein sequence (SEQ ID NO: 2), claims 1-7, 9-16, and 36-39 encompass numerous unknown and unidentified nucleic acids that have polynucleotide sequence adding to 5', 3' and/or within the nucleotide sequence of SEQ ID No. 1 or nucleic acids encoding various variants of SEQ ID No. 1 that miss from the disclosure. It is unclear whether these variants of SEQ ID No: 1 can still serve as a protein translation elongation factor as SEQ ID NO:1 does. Therefore, the general knowledge and level of skill in the art do not supplement the omitted description because specific, not general, guidance is what is needed.

Applicants have canceled claim 2, 3, 9, and 39, thus rendering the instant rejection moot as it pertains to these claims. With respect to claims 1, 4-6, 10-16, and 36-38, and new claims 40, 41, and 42, Applicants respectfully traverse the foregoing rejection and submit that there is sufficient written description in Applicants' specification regarding nucleic acid molecules comprising SEQ ID NO:1, nucleic acid molecules with a significant degree of homology to SEQ ID NO:1 and SEQ ID NO:2, and disrupted or modified nucleic acid molecules comprising SEQ ID NO:1, which encode polypeptides which are capable of functioning as protein translation elongations factor G polypeptides, to inform a skilled artisan that Applicants were in possession of the claimed invention at the time the application was filed as required by section 112, first paragraph (see M.P.E.P. 2163.02). In order to meet the written description requirement of the first paragraph of 35 U.S.C. §112, it is not necessary that a patent specification describe each and every specific member of a genus recited in a claim.

With respect to claim 1, the Examiner asserts that claim 1 is read to include "any kind of isolated nucleic acid molecule which had SEQ ID NO: 1 and was longer than the nucleotide sequence consisting of SEQ ID NO: 1, and could be read as a chromosome having SEQ ID NO: 1." Applicants respectfully submit that Applicants' specification at page 28, lines 7-11 defines the term isolated as follows:

> [a]n "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are

> present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived.

Accordingly, based on the above definition, the claimed isolated nucleic acid molecules of claim 1, which comprise SEQ ID NO:1 do not contain surrounding chromosomal DNA.

Furthermore, with respect to the remaining rejected claims 4-6, 10-16, and 36-38, and new claims 40, 41, and 42, a claim to a genus of chemical compounds satisfies the written description requirement when its accompanying specification either defines by sequence a representative number of its members falling within the scope of the genus or when its accompanying specification defines the structural features common to a substantial portion of the genus *(The Regents of the University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997)). For reasons discussed in detail below, the instant specification satisfies this requirement for the claimed invention.

The instant specification describes how modified or disrupted variants of SEQ ID NO:1 may be identified or produced and teaches what kind of sequence variation functional and non-functional variants of a polypeptide encoded by SEQ ID NO:1 may have (see, for example, page 27, lines 3-29).

Furthermore, claim 5 is not directed to any and/or all polynucleotides but rather are directed only to those which encode functional protein translation elongation factor G polypeptides that are encoded by a nucleic acid molecule with a high degree of identity to SEQ ID NO:1 and which hybridizes to a full complement of a nucleic acid molecule consisting of SEQ ID NO:1, in 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C. The recited stringent hybridization conditions determine a specific subgenus of molecules in accordance with the invention, *i.e.*, the subgenus of polynucleotides that encode polypeptides capable of functioning as a protein translation elongation factor G polypeptides.

Example 14 of the *Revised Interim Written Description Guidelines Training Materials* provides that a claim directed to variants of a polypeptide having SEQ ID

NO:3 "that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B" with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that "[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity."

Similarly, in the present case, claims 6 and 42 are directed to isolated nucleic acid molecules comprising or consisting of a nucleotide sequence that is at least 90% identical to the nucleotide sequence shown in SEQ ID NO:1, wherein the nucleotide sequence encodes a polypeptide capable of functioning as a protein translation elongation factor G polypeptide.

Applicants have disclosed in the instant specification assays for identifying all of the at least 90% identical variants of SEQ ID NO:1 which encode polypeptides capable of functioning as a protein translation elongation factor G polypeptide (see, for example, page 16, line 14 through page 15, line 24 and page 54, line 24 through page 55, line 13 of the specification). Thus, based on the teachings in Applicants' specification, one of skill in the art would conclude that Applicants were in possession of the claimed invention at the time of filing.

With respect to claim 7, which is directed to an isolated nucleic acid molecule which encodes a polypeptide fragment comprising at least 15 contiguous amino acid residues of the amino acid sequence of SEQ ID NO:2, Applicants have described various fragments of the polynucleotides of the invention.

In Example 15 of the *Interim Guidelines for Examination of Patent Applications Under the 35 U.S.C. §112, First Paragraph Written Description Requirement* the "theoretical specification" discloses a messenger RNA sequence, SEQ ID NO:1, which encodes a human growth hormone. The "theoretical specification" claims antisense

molecules that inhibit the production of human growth hormone. The Guidelines provide that

> [c]onsidering the specification's disclosure of (1) ***the sequence (SEQ ID NO:1) which defines and limits the structure of any effective molecules such that one skilled in the art would be able to immediately envisage members of the genus embraced by the claim*** and 2) the functional characteristics of the claimed invention as well as a routine art-recognized method of screening for antisense molecules which provide further distinguishing characteristics of the claimed invention, along with, 3) the general level of knowledge and skill in the art, one skilled in the art would conclude that applicant was in possession of the invention.....***the claimed invention is adequately described.***

Similar to Example 15 of the *Interim Guidelines*, the instant specification describes the nucleotide sequence of the nucleic acid molecules of the invention (SEQ ID NO:1) ***which define and limit the structure of any nucleotide fragments such that one skilled in the art would be able to immediately envisage members of the genus embraced by the nucleotide fragment claims***.

Moreover, as provided in Example 15 of the *Interim Guidelines*, the generation of oligonucleotide fragments is routine. For example, (as indicated in Example 15 of the *Interim Guidelines*) any specified fragment can be ordered from a commercial synthesizing service. Finally, Applicants' specification teaches how such polynucleotide fragments encoding polypeptides may be tested for activity (see, for example, page 40, lines 22-34 of the specification).

Based on the foregoing teachings in Applicants' specification and the knowledge generally available in the art, one skilled in the art would conclude that Applicants were in possession of the claimed invention at the time of filing of the application. The skilled artisan would also be able to make and use the claimed polypeptide fragments using only routine experimentation.

Accordingly, based on the amendments to the claims and the comments set forth above, Applicants respectfully request reconsideration and withdrawal of the instant rejection under 35 U.S.C. § 112, first paragraph.

Rejection of Claims 15 and 16 Under 35 U.S.C. §112, First Paragraph

The Examiner has rejected claims 15 and 16 under 35 U.S.C. §112, first paragraph, because, according to the Examiner

> the specification, while being enabling for modulating in production of certain kind of fine chemical using a nucleic acid molecule consisting of SEQ ID NO: 1, does not reasonably provide enablement for modulating in production of any kind of fine chemical recited in claims 15 and 16 in any kind of cell using a nucleic acid molecule comprising or consisting of SEQ ID NO:1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

Furthermore, the Examiner is of the opinion that

> the specification does not provide any evidence to show how a nucleic acid comprising or consisting of SEQ ID NO: 1 (protein translation elongation factor G, see Table 1) can modulate in production of any one of fine chemicals selected from claim 16 in any kind of cells. The evidence from an art search appears against the claimed invention as recited in claims 15 and 16. First, since it was well known in the art that protein synthesis in eukaryotes (i.e., animal cells) and prokaryotes (i.e. bacteria cells) required different ribosome subunits (see Text book of Biochemistry with Clinical correlations, edited by Thomas Devlin, third edition, 1992, page 725-727, specifically see Table 17.1), it is unclear whether a nucleic acid comprising or consisting of SEQ ID NO:1, a protein translation elongation factor G from *Corynebacterium glutamicum* (see Table 1), can interact with ribosome subunits from an eukaryote and modulate in production of any one of fine chemicals recited in claims 15 and 16 in an eukaryotic cell. Second, since conserved nucleotide sequences of the protein translation elongation factor G among bacteria were 41-85% (Caldon *et al,* Molecular microbiology, 41, 289-297, 2001, see Table 1), it is unclear whether a nucleic acid comprising or consisting of SEQ ID NO: 1 (protein translation elongation factor G from *Corynebacterium glutamicum)* can function in any kind of bacteria strain to modulate in production of any one of fine chemicals recited in claims 15 and 16. Third, it was known that disruption of certain kind of protein translation elongation factor in certain kind of cell did

> not affect survival of the cell. For example, disruption of ELF1 (an elongation like factor) in *Candida albicans* produced a mixture of large, irregular cells and apparently normal cells wherein the disrupted strains grew more slowly than wild-type (Sturtevant *et al,* Microbiology, 144, 2311-2321, see abstract) and disruption of GTPBP1 (elongation factor 1 alpha) in mice did not affect functions of antigen-present cells (Senju et al., Mol. Cell. Biol., 20, 6195-6200, 2000, see abstract). These evidence suggested that other protein translation elongation factor(s) can at least partially replace functions of the disrupted elongation factor and a protein translation elongation factor can not modulate in production of any kind of fine chemicals in a cell.

Applicants respectfully traverse the foregoing rejection and submit that Applicants' specification discloses ample guidance as to how one of skill in the art would make and use the claimed invention.

As the Examiner is aware, it is well known that enablement is not precluded by the necessity for some experimentation (see, *e.g.*, *In re Wands* 8 USPQ2d 1400-1407, 1404 (CAFC, 1988)). Applicants respectfully submit that any experimentation that may be required to select and/or make the claimed nucleic acid molecules, and subsequently practice methods of expressing and a polypeptide of the invention resulting in the production of a fine chemical constitutes routine, not undue, experimentation, and therefore the specification clearly enables the pending claims. Applicants specification clearly describes methods for transfecting various types of host cells including prokaryotic or eukaryotic cells, using various vectors (see, *e.g.,* page 38, line 30 through page 45, line 36 of Applicants' specification).

Furthermore, one of skill in the art would recognize that prokaryotic genes can function in eukaryotic cells as well as in prokaryotic cells other than the cell types to which the gene is endogenous. For example, as illustrated by the abstract attached hereto as Appendix A (Feher, *et al.* (1983) *Nature* 17-23;302(5905):266), bacterial genes are routinely expressed in yeast cells. Furthermore, the Examiner references a Text book of Biochemistry with Clinical correlations, edited by Thomas Devlin, third edition, 1992, page 725-727. Applicants respectfully submit that this reference states that "ribosome architecture has been highly conserved in evolution," and that "similarities between

ribosomes and subunits of different sources are more obvious than the differences." (see page 725). Accordingly, one would expect the translation elongation factor G of the instant invention to interact with various ribosomes.

Based on the foregoing, the skilled artisan would have been able to practice the claimed invention using only routine experimentation. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing rejection.

Rejection of Claims 36-38 Under 35 U.S.C. §112, Second Paragraph

The Examiner has rejected claims 36-38 under 35 U.S.C. 112, second paragraph, "as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention." In particular, the Examiner is of the opinion that claim 36 is "vague and indefinite because it is unclear whether the disrupted nucleic acid molecule can be still called as SEQ ID No. 1 since the claim does not limit the extent and percentage of the disruption."

Claim 37 is rejected as "vague and indefinite because it is unclear the nucleic acids with more modifications can be still called as SEQ ID No. 1 since the claim does not limit the extent and percentage of the modifications."

Claim 38 is rejected as "vague and indefinite because it is unclear the nucleic acids with modifications on its regulatory region can be still called as SEQ ID NO. 1 since the claim does not limit the extent and percentage of the modifications and it was known that the regulatory region of a nucleic acid molecule can locate anywhere of a genomic DNA."

Applicants respectfully traverse the foregoing rejection. However, in the interest of expediting prosecution and in no way conceding to the validity of the Examiner's position, claims 36, 37, and 38 have been amended such that they refer to the a nucleic acid molecule comprising a nucleotide sequence derived from SEQ ID NO:1, wherein the nucleic acid molecule is disrupted or modified, or wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule. In addition, claims 36, 37, and 38 have been amended such that they recite a function of the claimed nucleic acid molecule.

Based on the foregoing, Applicants respectfully submit that claims 36, 37, and 38, are clear and definite. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing rejection.

Rejection of Claims 1, 3, 6-9 and 39 Under 35 U.S.C. §102(b)

The Examiner has rejected claims 1, 3, 6-9 and 39 under 35 U.S.C. 102(b) "as being anticipated by New England Biolabs (1996/1997 Catalog, pages 113, 114, 164, and 165)." In particular, the Examiner is of the opinion that

> [r]egarding claims 1, 3, 6, 7, and 39, #1079 of the Catalog of New England Biolabs disclosed the linker of restriction enzyme ApaI with nucleotides 5'-GGGGCCCC-3' (page 113). Since nucleotides 50-57 of SEQ ID NO: 1 was CCCCGGTA (5' to 3'), the linker of restriction enzyme ApaI was considered as a complement of SEQ ID No: 1 as recited in claims 1 and 3, and a) and (b) of claim 39, a complement of an isolated nucleic acid molecule comprising a nucleotide sequence which has at least 50% identity of SEQ ID NO: 1 as recited in claim 6 and (e) of claim 39, and a complement of an isolated nucleic acid molecule comprising a fragment of at least 15 nucleotide of SEQ ID NO: 1 as recited in claim 7 and (f) of claim 39 because it had a portion of SEQ ID No: 1. Note that SEQ ID NO: 1 was at least 50% identity (100%) of SEQ ID NO: 1.
>
> Regarding claim 8, the linker of restriction enzyme ApaI (5'-GGGGCCCC-3') was capable of hybridizing with nucleotides 50-57 of SEQ ID NO: 1 (5'-CCCCGGTA-3') with 75% base match. Since the specification defines "under stringent conditions" as "conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other (see page 34, lines 3-8), the linker of restriction enzyme ApaI (5'-GGGGCCCC-3') was considered to be capable of hybridizing with nucleotides 50-57 of SEQ ID NO: 1 (5'-CCCCGGTA-3) under stringent conditions.
>
> Regarding claim 9, pMal vector comprised a polylinker and a lacZa gene (see page 165). Since a nucleotide connected with the first nucleotide of 5' lacZalpha gene in the polylinker and the lacZa gene were considered as a portion of SEQ ID NO: 1 and a nucleotide sequence encoding a heterologous polypeptide respectively, the pMal vector was considered to comprise a portion of SEQ ID NO: 1 and a nucleotide sequence encoding a heterologous polypeptide recited in claim 9.

Applicants have canceled claim 2, 3, and 39, thus rendering the instant rejection moot as it pertains to these claims. With respect to claims 1, 6, and 7, Applicants respectfully traverse the foregoing rejection for the following reasons.

For a prior art reference to anticipate a claimed invention, the prior art must teach each and every element of the claimed invention. *Lewmar Marine v. Barient* 827 F.2d 744, 3 USPQ2d 1766 (Fed. Cir. 1987).

Claim 1, as amended, is directed to an isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, or a full complement thereof. Claim 6, as amended, is directed to an isolated nucleic acid molecule comprising a nucleotide sequence which has at least 90% identity with the nucleotide sequence of SEQ ID NO:1, or a full complement thereof, and wherein said nucleic acid molecule encodes a polypeptide which is capable of functioning as a protein translation elongation factor G polypeptide. Claim 7, as amended, is directed to an isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO:1, or a full complement thereof.

The sequence set forth in the New England Biolabs Catalog cited by the Examiner is an eight nucleotide sequence. This sequence does not comprise the full complement of SEQ ID NO:1, as is claimed in claim 1. Accordingly, the sequences disclosed in the New England Biolabs Catalog do not teach each and every limitation of claim 1.

The a sequence alignment of the ***entire length*** of the nucleotide sequence disclosed by the New England Biolabs Catalog cited by the Examiner with the full complement of SEQ ID NO:1 would result in an extremely low percent identity than the percent similarity claimed in the instant application, *e.g.,* 90% identity. Accordingly, the sequences disclosed in the New England Biolabs Catalog do not teach each and every limitation of claim 6.

With respect to claim 7, Applicants respectfully submit that the New England Biolabs Catalog does not disclose a nucleotide sequence encoding a polypeptide fragment comprising ***at least*** 15 contiguous amino acid residues of the amino acid sequence of SEQ ID NO:2. Therefore, the New England Biolabs Catalog does not teach each and every

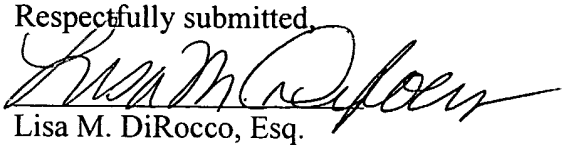
limitation of claim 7. Accordingly, Applicants respectfully request reconsideration and withdrawal of the instant 35 U.S.C. §102(b) rejection.

Based on the reasons set forth above, Applicants respectfully request that the Examiner reconsider and withdraw the foregoing rejection under 35 U.S.C. §102.

SUMMARY

If a telephone conversation with Applicants' Attorney would expedite the prosecution of the above-identified application, the examiner is urged to call the undersigned at (617) 227-7400.

Respectfully submitted,



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